



IFW16

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/390,846**

**DATE: 08/27/2004**  
**TIME: 10:15:26**

**Input Set : N:\Crf3\RULE60\09390846.raw**  
**Output Set: N:\CRF4\08272004\I390846.raw**

**SEQUENCE LISTING**

## 3 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Kok, Jacobus Johannes  
 van den Boogaart, Paul  
 Vermeulen, Arnoldus Nicolaas

11 (ii) TITLE OF INVENTION: Coccidiosis poultry vaccine

14 (iii) NUMBER OF SEQUENCES: 2

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Akzo Nobel Patent Department  
 19 (B) STREET: 1300 Piccard Drive, Suite 206  
 20 (C) CITY: Rockville  
 21 (D) STATE: Maryland  
 22 (E) COUNTRY: USA  
 23 (F) ZIP: 20850

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Floppy disk  
 28 (B) COMPUTER: IBM PC compatible  
 29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

33 (vi) CURRENT APPLICATION DATA:

C--> 34 (A) APPLICATION NUMBER: US/09/390,846  
 C--> 35 (B) FILING DATE: 14-Sep-1999

36 (C) CLASSIFICATION:

38 (vii) PRIOR APPLICATION DATA:

39 (A) APPLICATION NUMBER: US/08/676,882  
 40 (B) FILING DATE: 03-JUL-1996

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Gormley, Mary E.  
 44 (B) REGISTRATION NUMBER: 34,409

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: (301) 258-5200  
 49 (B) TELEFAX: (301) 977-0847

52 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 1679 base pairs  
 57 (B) TYPE: nucleic acid  
 58 (C) STRANDEDNESS: double  
 59 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: cDNA to mRNA

65 (iii) HYPOTHETICAL: NO

68 (iv) ANTI-SENSE: NO

71 (vi) ORIGINAL SOURCE:

72 (A) ORGANISM: *Eimeria acervulina*

ENTERED

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73 (D) DEVELOPMENTAL STAGE: Schizont  
 76 (vii) IMMEDIATE SOURCE:  
 77 (B) CLONE: EASC2\_1  
 80 (ix) FEATURE:  
 81 (A) NAME/KEY: CDS  
 82 (B) LOCATION:280..1269  
 83 (D) OTHER INFORMATION:/function= "Eimeria lactate  
 84 dehydrogenase"  
 87 (ix) FEATURE:  
 88 (A) NAME/KEY: misc\_feature  
 89 (B) LOCATION:1..51  
 90 (D) OTHER INFORMATION:/label= pBluescriptII  
 93 (ix) FEATURE:  
 94 (A) NAME/KEY: misc\_feature  
 95 (B) LOCATION:1624..1679  
 96 (D) OTHER INFORMATION:/label= pBluescriptII  
 99 (ix) FEATURE:  
 100 (A) NAME/KEY: misc\_feature  
 101 (B) LOCATION:45..54  
 102 (D) OTHER INFORMATION:/label= EcoRI-linker  
 105 (ix) FEATURE:  
 106 (A) NAME/KEY: misc\_feature  
 107 (B) LOCATION:1621..1630  
 108 (D) OTHER INFORMATION:/label= EcoRI-linker  
 112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 114 GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT CCCCCGGGCT GCAGGAATTG GGGT  
 117 TTTTTTTCT ACACATTAAT ATTCTTCGTT TACGTTTATT TTGCTACAAA TAAA  
 120 AAACTCTCTA TTTCCTCATA TTCTACCAGCT TCATCGTGG GTGTGTAAGA CGTA  
 123 TACAGCTGGG GCTGGCTTAC TGCGCACCGC TTATTTATTA CTTAATTCTACAC  
 126 TATCTTTCTT CTTCTTTTTT CTTGCTCTTT CTTGTGAAA ATG GCG GTC TTC  
 127 Met Ala Val Phe  
 128 1  
 131 AAG AAT ACA CGC CCC AAG ATT GCT ATG GTG GGC TCC GGT ATG ATT  
 132 Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly Ser Gly Met Ile  
 133 10 15 20  
 136 GGC ACC ATG GCT TTC CTG TGC AGC TTG AGG GAA CTC GGA GAT GTT  
 137 Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu Leu Gly Asp Val  
 138 25 30 35  
 141 CTC TTC GAC GTT GTA CCG AAC ATG CCG ATG GGG AAG GCG ATG GAT  
 142 Leu Phe Asp Val Val Pro Asn Met Pro Met Gly Lys Ala Met Asp  
 143 40 45 50  
 146 TCG CAC AAT TCG TCG GTG GTT GAC ACG GGT ATA ACA GTA TAC GGC  
 147 Ser His Asn Ser Ser Val Val Asp Thr Gly Ile Thr Val Tyr Gly  
 148 55 60 65  
 151 AAT TCA TAC GAG TGC TTG AAG GGT GCG GAC GTA GTA ATA ATA ACA  
 152 Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val Val Ile Ile Thr  
 153 70 75 80  
 156 GGG ATA ACA AAG ATA CCC GGA AAG AGC GAT AAA GAA TGG TCT AGA  
 157 Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys Glu Trp Ser Arc

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158	90	95	100	
161	GAT CTA TTA CCT GTG AAT ATA AAG ATA ATG AGG GAG GTC GGT GCA GCA			630
162	Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg Glu Val Gly Ala Ala			
163	105	110	115	
166	ATT AAA TCT TAC TGT CCT AAT GCA TTT GTT ATT AAT ATA ACA AAT CCT			678
167	Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile Asn Ile Thr Asn Pro			
168	120	125	130	
171	TTA GAT GTG ATG GTA GCT GCT CTT CAA GAG TCA TCA GGA CTA CCT CAT			726
172	Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser Ser Gly Leu Pro His			
173	135	140	145	
176	CAT AGA ATC TGC GGT ATG GCT GGG ATG CTT GAT AGC TCT CGT TTT AGA			774
177	His Arg Ile Cys Gly Met Ala Gly Met Leu Asp Ser Ser Arg Phe Arg			
178	150	155	160	165
181	CGT ATG ATA GCT GAT AAA TTA GAA GTC TCT CCT AGA GAT GTA CAG GGG			822
182	Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro Arg Asp Val Gln Gly			
183	170	175	180	
186	ATG GTC ATA GGT GTA CAC GGC GAT CAT ATG GTG CCC CTA AGT AGA TAT			870
187	Met Val Ile Gly Val His Gly Asp His Met Val Pro Leu Ser Arg Tyr			
188	185	190	195	
191	GCA ACA GTT AAC GGC ATC CCG CTT TCT GAG TTT GTT AAG AAG GGC TGG			918
192	Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe Val Lys Lys Gly Trp			
193	200	205	210	
196	ATC AAG CAA GAA GAA GTA GAT GAT ATC GTT CAG AAG ACC AAG GTC GCT			966
197	Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln Lys Thr Lys Val Ala			
198	215	220	225	
201	GGA GGA GAG ATC GTA CGC CTA TTA GGA CAA GGC TCT GCT TAC TAT GCT			1014
202	Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly Ser Ala Tyr Tyr Ala			
203	230	235	240	245
206	CCA GGG GCT TCA GCT ATT CAG ATG GCT GAG AGC TAT CTA AAG GAT AGA			1062
207	Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser Tyr Leu Lys Asp Arg			
208	250	255	260	
211	AAG AGA GTG ATG GTT TGC TCT TGC TAC TTG CAA GGA CAA TAT GGT GTA			1110
212	Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln Gly Gln Tyr Gly Val			
213	265	270	275	
216	CAG AAT CAC TAC TTA GGA GTA CCT TGT GTT ATC GGT GGG AGA GGT GTT			1158
217	Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile Gly Gly Arg Gly Val			
218	280	285	290	
221	GAG AAG ATT ATT GAG TTA GAA TTG ACC GCA CAA GAA AGA CAG GAG CTT			1206
222	Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln Glu Arg Gln Glu Leu			
223	295	300	305	
226	CAG GGA TCT ATC GAT GAG GTT AAG GAG ATG CAG AAG GCT ATT GCT GCT			1254
227	Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln Lys Ala Ile Ala Ala			
228	310	315	320	325
231	CTT GAT GCA TCC AAG TAAGCAGCAG CAAAATCGCA GAAGTTGCAG CGCTAGAAC			1309
232	Leu Asp Ala Ser Lys			
233	330			
236	ACCAGCAGCA GCAGCAGCAG CAGCCTATAG TTCTTGCTGC TGCTGTTCCCT ACTACAGCTG			1369
239	CGGCTTTCTT CCTCGTGTAA TTATCATGAT AGTAAGCTGC TGTACCAGCA GCAGCAGCAG			1429
242	CAGCAGATTG TGCTTGACCC GCCGTTGTT TTGCGTACAC CGGCAGAAAT ATTGACTTGC			1489

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245	AGTTAGGAGA AAGAAAGAAA ACAAACACGA TCCCATCGAT CCCAATAAAC CCCACACTGT	1549
248	CGATCCCATC GATCCCAGCA ACTCCACGGG GCTCTTAAC GTTAAACCTA TTATTCTTAT	1609
251	CATTACTGTC TCCCGAATTC GATATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGC	1669
254	CCGGTACCCA	1679

257 (2) INFORMATION FOR SEQ ID NO: 2:

260 (i) SEQUENCE CHARACTERISTICS:  
261 (A) LENGTH: 330 amino acids  
262 (B) TYPE: amino acid  
263 (D) TOPOLOGY: linear

267 (ii) MOLECULE TYPE: protein

271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

275	Met Ala Val Phe Glu Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly	
276	1 5 10 15	
279	Ser Gly Met Ile Gly Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu	
280	20 25 30	
283	Leu Gly Asp Val Val Leu Phe Asp Val Val Pro Asn Met Pro Met Gly	
284	35 40 45	
287	Lys Ala Met Asp Ile Ser His Asn Ser Ser Val Val Asp Thr Gly Ile	
288	50 55 60	
291	Thr Val Tyr Gly Ser Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val	
292	65 70 75 80	
295	Val Ile Ile Thr Ala Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys	
296	85 90 95	
299	Glu Trp Ser Arg Met Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg	
300	100 105 110	
303	Glu Val Gly Ala Ala Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile	
304	115 120 125	
308	Asn Ile Thr Asn Pro Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser	
309	130 135 140	
313	Ser Gly Leu Pro His His Arg Ile Cys Gly Met Ala Gly Met Leu Asp	
314	145 150 155 160	
318	Ser Ser Arg Phe Arg Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro	
319	165 170 175	
323	Arg Asp Val Gln Gly Met Val Ile Gly Val His Gly Asp His Met Val	
324	180 185 190	
328	Pro Leu Ser Arg Tyr Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe	
329	195 200 205	
333	Val Lys Lys Gly Trp Ile Lys Gln Glu Val Asp Asp Ile Val Gln	
334	210 215 220	
338	Lys Thr Lys Val Ala Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly	
339	225 230 235 240	
343	Ser Ala Tyr Tyr Ala Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser	
344	245 250 255	
348	Tyr Leu Lys Asp Arg Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln	
349	260 265 270	
353	Gly Gln Tyr Gly Val Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile	
354	275 280 285	
357	Gly Gly Arg Gly Val Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln	
358	290 295 300	

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362 Glu Arg Gln Glu Leu Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln  
363 305 310 315 320  
367 Lys Ala Ile Ala Ala Leu Asp Ala Ser Lys  
368 325 330

**VERIFICATION SUMMARY**

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L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]